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Figure 1

1 GAATTCGCGGCCGCGTCGACAGATGCCTTCTTCTGCCTGAGATTACACCCCACTAGCCAA 60

61 CCACTTTTGCCTTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGCTCACCTGG 120

121 ACCCGACTGCCCAAGGGTCAAGAACTCCCCGACCATCTTGACGAAGCCCTACACAGG 180

181 GACCTGGCCAACCTCAGGATCCAACACCCCTCAGGTGACCCCTCCTCCAGTACGTGGATGAC 240

241 CTGCTTCTGGCGGGAGCCACCAAACAGGACTGCTTAGAAGGTACGAAGGCACTAUTGCTG 300

301 GAATTGTCTGACCTAGGCTACAGAGCCTCTGCTAAGAAGGCCAGATTGCAAGGAGAG 360

361 GTAACATACTGGGTACAGTTGCAGGGGGCAGCGATGGCTGACGGAGGCACGGAAAG 420

421 AAAACTGTAGTCCAGATAACCGGCCCAACCACAGCCAAACAAGTGAGAGAGTTTGGGG 480

481 ACAGCTGGATTTGCAGACTGTGGATCCCGGGTTGCGACCTTAGCAGCCCCACTCTAC 540

541 CCGCTAACCAAAGAAAAGGGGGATTCTCCTGGCCTGAGCACCAGAAGGCATTGAT 600

601 GCTATCAAAAGGCCCTGCTGAGCCACCTGCTCTGGCCCTCCCTGACGTAACAAACCC 660

661 TTTACCCCTTATGTGGATGAGCGTAAGGGAGTAGCCCGAGGAGTTAACCAAACCTA 720

721 GGACCATGGAGGAGACCTGTTGCCTACCTGTCAAAGAAGCTTGATCCTGTAGCCAGTGGT 780

781 TGGCCCGTATGTCTGAAGGCTATCGCAGCTGTGGCCATACTGGTCAAGGACGCTGACAAA 840

841 TTGACTTTGGACAGAATATAACTGTAATAGCCCCCATGCATTGGAGAACATCGTCGG 900

901 CAGCCCCCAGACCGATGGATGACCAACGCCCGCATGACCCACTATCAAAGCCTGCTTCTC 960

961 ACAGAGAGGGTCACTTGCTCCACCAGCCGCTCTCAACCCCTGCCACTCTTGCTGAA 1020

1021 GAGACTGATGAACCAGTGACTCATGATTGCCATCAACTATTGATTGAGGAGACTGGGTC 1080

1081 CGCAAGGACCTTACAGACATAACCGCTGACTGGAGAAGTGCTAACCTGGTTCACTGACGGA 1140

1141 AGCAGCTATGTGGTGGAAAGGTAAAGAGGATGGCTGGGGCGGAGTGGTGGACGGGACCCGC 1200

1201 ACGATCTGGGCCAGCAGCCTGCCGGAGGAACCTCAGCGAAAAGGCTGAGCTCATGGCC 1260

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Figure 1 cont.

1261	CTCACGCAAGCTTGC GGCTGGCGAAGGGAAATCCATAAACATTTACGGACAGCAGG	1320
1321	TATGCCTTGCGACTGCACACGTACACGGGCCATCTATAAACAAAGGGGTTGCTTACC	1380
1381	TCAGCAGGGAGGGAAATAAAGAACAAAGAGGGAAATTCTAAGCCTATTAGAAGCCTTACAT	1440
1441	TTGCCAAAAAGGCTAGCTATTATACTGTCCTGGACATCAGAAAGCCAAGATCTCATA	1500
1501	TCTAGAGGGAACAGATGGCTGACCGGGTTGCCAAGCAGGCAGGCCAGGCTGTTAACCTT	1560
1561	CTGCCTATAATAGAAACGCCAAAGCCCAGAACCCAGACGACAGTACACCCCTAGAACAGAC	1620
1621	TGGCAAGAGATAAAAAGATAGACCAGTTCTCTGAGACTCCGGAGGGACCTGCTATACC	1680
1681	TCATATGGGAAGGAAATCCTGCCCAACAAAGAAGGGTTAGAATATGTCCAACAGATACT	1740
1741	CGTCTAACCCACCTAGGAACTAAACACCTGCAGCAGTTGGTCAGAACATCCCCTATCAT	1800
1801	GTTCTGAGGCTACCAGGAGTGGCTGACTCGGTGGTCAAACATTGTGTGCCCTGCCAGCTG	1860
1861	GTAAATGCTAATCCTCCAGAATACCTCCAGGAAAGAGACTAAGGGGAAGCCACCCAGGC	1920
1921	GCTCACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGAAACAAATATCTA	1980
1981	TTGGTTTTGTAGACACCTTTCAGGATGGTAGAGGGCTTATCCTACTAAGAAAGAGACT	2040
2041	TCAACCGTGGTGGCTAAGAAAATCTGGAGGAAATTTCAGGATTTCCAAGATTTGGAATACCTAAG	2100
2101	GTAATAGGGTCAGACAATGGTCCAGCTTCGTTGCCAGGTAAGTCAGGGACTGCCAAG	2160
2161	ATATTGGGATTGATTGGAAACTGCATTGTGCATAAGACCCAAAGCTCAGGACAGGTA	2220
2221	GAGAGGATGAATAGAACCATAAAGAGACCCCTACCAAATTGACCACAGAGACTGGCATT	2280
2281	AATGATTGGATGGCTCTCCTGCCCTTGTGCTTTAGGGTAGGAACACCCCTGGACAG	2340
2341	TTTGGGCTGACCCCTATGAATTGCTCTACGGGGACCCCCCGTTGGCAGAAATTGCC	2400
2401	TTTGCACATAGTGCTGATGTGCTGCTTCCAGCCTTGTCTAGGCTCAAGGCGCTC	2460
2461	GAGTGGGTGAGGCAGCGAGCGTGGAAAGCAGCTCCGGAGGCCTACTCAGGAGGAGACTTG	2520

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Figure 1 cont.

2521	CAAGTTCCACATCGCTTCCAAGTTGGAGATTCACTCTATGTTAGACGCCACCGTCAGGA	2580
2581	AACCTCGAGACTCGGTGGAAGGGACCTTATCTCGTACTTTGACCACACCAACGGCTGTG	2640
2641	AAAGTCGAAGGAATCCCCACCTGGATCCATGCATCCCACGTTAAGCCGGCGCCACCTCCC	2700
2701	GATTGGGGTGGAAAGCCGAAAAGACTGAAAATCCCTTAAGCTTCGCCTCCATCGCTG	2760
2761	GTTCCCTTACTCTGTCAATAACTCCTCAAGTTAATGGTAAACGCCCTGTGGACAGCCCGAA	2820
2821	CTCCCATAAACCTTATCTCACCTGGTTACTTACTGACTCCGGTACAGGTATTAAATAT	2880
2881	TAACAGCACTCAAGGGAGGCTCCCTGGGACCTGGTGGCCTGAATTATATGTCTGCCT	2940
2941	TCGATCAGTAATCCCTGGTCTCAATGACCAGGCCACACCCCCCGATGTACTCCGTGCTTA	3000
3001	CGGGTTTACGTTGCCAGGACCCCCAAATAATGAAGAATATTGTGAAATCCTCAGGA	3060
3061	TTTCCTTGCAAGCAATGGAGCTGCATAACTCTAATGATGGGAATTGAAATGCCAGT	3120
3121	CTCTCAGCAAGACAGAGTAAGTTACTCTTGTAAACAATCCTACCAAGTTATAATCAATT	3180
3181	TAATTATGCCATGGAGATGGAAAGATTGGCACAGCGGGTACAAAAAGATGTACGAAA	3240
3241	TAAGCAAATAAGCTGTCATTGTTAGACCTAGATTACTTAAAAATAAGTTCACTAAAAA	3300
3301	AAAAAAAAAAAAAAAAAAAAA 3320	

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Figure 2

1 TGTGGCCCCAGCGCGCTTGGAAATAAAAATCCTCTTGCTGTTGCATCAAGACCGCTTCT 60  
 61 CGTGAGTGATTGGGGTGTGCCCTCTCCGAGCCCGGACGAGGGGGATTGTTCTTTACT 120  
 121 GGCCTTCATTGGTGCCTGGCCGGAAATCCTGCGACCACCCCTAACACCGAGAAC 180  
 181 GACTTGGAGGTAAAGGGATCCCCTTGGAACGTGTGTGTGTGGCCGGCGTCTGT 240  
 241 CTGAGTGTCTGTTTGGTGAATGCGCGCTTCGGTTGCAGCTGTCTCAGACCGTAA 300  
 301 GGACTGGAGGACTGTGATCAGCAGACGTGCTAGGAGGATCACAGGCTGCCACCCGGGG 360  
 361 ACGCCCCGGAGGTGGGAGAGGCCAGGGACGCCCTGGTGGTCTCCTACTGTGGTCAGAGG 420  
 421 ACCGAGTTCTGTTGTAAGCGAAAGCTTCCCCCTCCGGCCGTCCACTCTTTGCCT 480  
 481 GCTTGTGGAAGACCGGGACGGGTCGCGTGTGTCTGGATCTGTTGGTTCTGTCTCGTGT 540  
 541 TCTTTGTCTTGTGCGTCCTGTCTACAGTTAATATGGGACAGACAGTGAACCCCC 600  
 601 TTAGTTGACTCTGACCATTGGACTGAAGTTAGATCCAGGGCTCATATTGTCAAGTTC 660  
 661 AGGTTAAGAAGGGACCTTGGCAGACTTCTGTGCCTCTGAATGGCAAACATTGATGTTG 720  
 721 GATGGCCATCAGAGGGGACCTTAATTCTGAAATTATCCTGGCTGTTAAGGCAATCATT 780  
 781 TTCAGACTGGACCCGGCTCTCATCCTGATCAGGAGCCCTATATCCTTACGTGGCAAGATT 840  
 841 TGGCAGAAGATCCTCCGCCATGGTTAAACCATGGCTAAATAACCAAGAAAGCCAGGTC 900  
 901 CCCGAATCCTGGCTTTGGAGAGAAAAACAAACACTCGGCCGAAAAAGTCGAGCCCTCTT 960  
 961 CCTCGTATCTACCCGAGATCGAGGAGCCGACTTGGCCGGAACCCAACCTGTTCCC 1020  
 1021 CCACCCCCCTATCCAGCACAGGTGCTGTGAGGGGACCTCTGCCCTCTGGAGCTCCGG 1080  
 1081 TGGTGGAGGGACCTGCTGCCGGACTCGGAGCCGGAGAGGCGCCACCCGGAGCGGGACAG 1140  
 1141 ACGAGATCGCGATATTACCGCTGCGCACCTATGGCCCTCCCATGCCAGGGGCCATTGC 1200  
 1201 AGCCCTCCAGTATTGGCCCTTTCTCTGCAGATCTCTATAATTGGAAAACTAACCATC 1260

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Figure 2 cont.

1261	CCCCTTCTCGGAGGGATCCCCAACGCCTCACGGGTTGGTGGAGTCCTTATGTTCTCTC	1320
1321	ACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCACAACCGAGGGAGC	1380
1381	GAGAGAGAATTCTGTTAGAGGCTAGAAAAAAATGTTCTGGGCCGACGGCGACCCACGC	1440
1441	AGTTGCAAAATGAGATTGACATGGGATTCCTTGA CTCGCCCCGGTTGGGACTACAACA	1500
1501	CGGCTGAAGGTAGGGAGAGCTTGAAAATCTATGCCAGGCTCTGGTGGCGGGCTCCGGG	1560
1561	GCGCCTCAAGACGGCCCCTAAATTGGCTAAGGTAAGAGAGGGTGTGCAGGGACCGAACG	1620
1621	AACCTCCCTCGGTATTCCTTGAGAGGCTCATGGAAGCCTTCAGGCCGGTCAACCCCTTTG	1680
1681	ATCCTACCTCAGAGGCCAGAAAGCCTCAGTGGCCCTGGCCTTCATTGGCAGTCGGCTC	1740
1741	TGGATATCAGGAAGAACTTCAGAGACTGGAAGGGTTACAGGAGGCTGAGTTACGTGATC	1800
1801	TAGTGAGAGAGGCAGAGAAGGTGTATTACAGAAGGGAGACAGAAGAGGAGAAGGAACAGA	1860
1861	GAAAAGAAAAGGGAGAGAGAAGAAAGGGAGGAAGACGTGATAGACGGCAAGAGAAATT	1920
1921	TGACTAAGATCTTGGCCGCAGTGGTTGAAGGGAAAGAGCAGCAGGGAGAGAGAGAGATT	1980
1981	TTAGGAAAATTAGGTCAAGGCCCTAGACAGTCAGGGAACCTGGCAATAGGACCCACTCG	2040
2041	ACAAGGACCAGTGTGCGTATTGTAAGAAAAAGGACACTGGCAAGGAAGTGCCTTAAAGA	2100
2101	AGGGAAACAAAGGACCGAAGTCCTAGCTCTAGAAGAAGATAAAGATTAGGGAGACGGGT	2160
2161	TCGGACCCCTCCCCGAGCCAGGGTAACCTTGAAAGGTGGAGGGCAACCAGTTGAGTTC	2220
2221	CTGGTTGATACCGGAGCGGAGCATTCACTGCTGCTACAACCATTAGGAAAAGTAAAGAA	2280
2281	AAAAAAATCCTGGGTGATGGGTGCCACAGGGCAACGGCAGTATCCATGGACTACCGAAGA	2340
2341	ACCGTTGACTTGGGAGTGGGACGGGTAACCCACTCGTTCTGGTCATCCCTGAGTGCCTA	2400
2401	GTACCCCTCTAGGTAGAGACTTACTGACCAAGATGGAGCTAAATTCTTTGAACAA	2460
2461	GGAAGACCAGAAGTGTCTGTGAATAACAAACCCATCACTGTGTTGACCCCTCCAATTAGAT	2520

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Figure 2 cont.

2521	GATGAATATCGACTATATTCTCCCCAAGTAAAGCCTGATCAAGATATAACAGTCCTGGTTG	2580
2581	GAGCAGTTCCCCAAGCCTGGCAGAAACCGCAGGGATGGGTTGGCAAAGCAAGTTCCC	2640
2641	CCACAGGTTATTCAACTGAAGGCCAGTGCTACACCACTATCAGTCAGACAGTACCCCTG	2700
2701	AGTAGAGAGGCTCGAGAAGGAATTGGCCGCATGTTCAAAGATTAATCCAACAGGGCATC	2760
2761	CTAGTT CCTGTCCAATCCCCTTGGAAATACTCCCCTGCTACCGGTTAGGAAGCCTGGGACC	2820
2821	AATGATTATCGACCACTACAGGACTTGAGAGAGGTCAATAAAAGGGTGCAGGACATACAC	2880
2881	CCAACGGTCCCGAACCCCTTATAACCTCTTGAGCGCCCTCCGGCTGAACGGAACGGTAC	2940
2941	ACAGTATTGGACTAAAAGATGCCTTCTTCTGCCTGAGATTACACCCACTAGCCAACCA	3000
3001	CTTTTGCCCTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGCAGCTCACCTGGACC	3060
3061	CGACTGCCCAAGGGTTCAAGAACTCCCCGACCATCTTGACGAAGCCCTACACAGGGAC	3120
3121	CTGGCCAACCTCAGGATCCAACACCCCTCAGGTGACCCCTCCAGTACGTGGATGACCTG	3180
3181	CTTCTGGCGGGAGCCAAACAGGACTGCTTAGAAGGTACGAAGGCACTACTGCTGGAA	3240
3241	TTGTCTGACCTAGGCTACAGAGCCTCTGCTAAGAAGGCCAGATTGAGGAGAGGTA	3300
3301	ACATACTGGGTACAGTTGGGGGGGGCAGCGATGGCTGACGGAGGCACGGAAAGAAA	3360
3361	ACTGTAGTCCAGATACCGGCCCCAACACAGCCAAACAAGTGAGAGAGTTTGGGACA	3420
3421	GCTGGATTTGCAGACTGTGGATCCGGGGTTGCGACCTAGCAGCCCCACTCTACCCG	3480
3481	CTAACCAAAAGAAAAAGGGGGATTCTCCTGGCTCCTGAGCACCAGAAGGCAATTGATGCT	3540
3541	ATCAAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACGTAACAAACCTTT	3600
3601	ACCCTTATGTGGATGAGCGTAAGGGAGTAGCCCGAGGAGTTAACCCAAACCTAGGA	3660
3661	CCATGGAGGAGACCTGTTGCCTACCTGTCAAAGAAGCTTGTAGCCAGTGGTTGG	3720
3721	CCCGTATGTGAAGGCTATCGCAGCTGTGGCCATACTGGTCAAGGACGCTGACAAATTG	3780

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Figure 2 cont.

3781	ACTTTGGGACAGAATATAACTGTAATAGCCCCCATGCATTGGAGAACATCGTCGGCAG	3840
3841	CCCCCAGACCGATGGATGACCAACGCCGCATGACCCACTATCAAAGCCTGCTTCTCAC	3900
3901	GAGAGGGTCACTTCGCTCCACCAGCCGCTCTCAACCCTGCCACTCTTCTGCCTGAAGAG	3960
3961	ACTGATGAACCAGTGACTCATGATTGCCATCAACTATTGATTGAGGAGACTGGGTCCGC	4020
4021	AAGGACCTTACAGACATAACCGCTGACTGGAGAAGTGCTAACCTGGTTACTGACGGAAGC	4080
4081	AGCTATGTGGTGGAAAGGTAAGAGGGATGGCTGGGGGGCAGTGGTGGACGGGACCCGACG	4140
4141	ATCTGGGCCAGCAGCCTGCCCGGAAGGAACCTCAGCGAAAAGGCTGAGCTCATGGCCCTC	4200
4201	ACGCAAGCTTGGCGCTGGCGAAGGGAAATCCATAAACATTATACGGACAGCAGGTAT	4260
4261	GCCTTGCAGTGCACACGTACACGGGCCATCTATAAACAAAGGGGTTGCTTACCTCA	4320
4321	GCAGGGAGGGAAATAAGAACAAAGAGGGAAATTCTAAGCCTATTAGAACCTTACATTG	4380
4381	CCAAAAAAGGCTAGCTATTATACACTGTCCTGGACATCAGAAAGCCAAAGATCTCATATCT	4440
4441	AGAGGGAAACCAGATGGCTGACCGGGTTGCCAAGCAGGCAGCCCAGGCTGTTAACCTCTG	4500
4501	CCTATAATAGAAACGCCAAGCCCCAGAACCCAGACAGTACACCTAGAACAGACTGG	4560
4561	CAAGAGATAAAAAGATAGACCAAGTCTCTGAGACTCCGGAGGGACCTGCTATAACCTCA	4620
4621	TATGGGAAGGAAATCTGCCAACAAAAGAAGGGTTAGAATATGTCCAACAGATACTCGT	4680
4681	CTAACCCACCTAGGAACCTAACACCTGCAGCAGTTGGTCAGAACATCCCCTATCATGTT	4740
4741	CTGAGGCTACCAGGAGTGGCTGACTCGGTGGTCAAACATTGTGTGCCCTGCCAGCTGGTT	4800
4801	AATGCTAATCCTCCAGAATACCTCCAGGAAAGAGAGACTAAGGGGAAGCCACCCAGGCGCT	4860
4861	CACTGGGAAGTGGACTTCACTGAGGTAAAGCCGGCTAAATACGGAAACAAAATATCTATTG	4920
4921	GTTTTGTAGACACCTTTCAGGATGGTAGAGGGTTATCCTACTAAGAAAGAGACTTCA	4980
4981	ACCGTGGTGGCTAAGAAAATCTGGAGGAAATTTCAGAAGATTGGAATACCTAAGGT	5040

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Figure 2 cont.

5041	ATAGGGTCAGACAATGGTCCAGCTTCGTTGCCAGGTAAGTCAGGGACTGGCCAAGATA	5100
5101	TTGGGGATTGATTGGAAACTGCATTGTGCATAACAGACCCCAAAGCTCAGGACAGGTAGAG	5160
5161	AGGATGAATAGAACCATTAAGAGAGACCCCTAACCAATTGACCACAGAGACTGGCATTAAAT	5220
5221	GATTGGATGGCTCTCCTGCCCTTGTGCTTTAGGGTGAGGAACACCCCTGGACAGTT	5280
5281	GGGCTGACCCCCCTATGAATTGCTCTACGGGGACCCCCCCCCTGGCAGAAAATTGCCCTT	5340
5341	GCACATAGTGCTGATGTGCTGCTTCCCAGCCTTGTCTAGGCTCAAGGCCTCGAG	5400
5401	TGGGTGAGGCAGCGAGCGTGGAAAGCAGCTCCGGAGGCCTACTCAGGAGGAGACTTGCAA	5460
5461	GTTCCACATCGCTTCCAAGTTGGAGATTCACTATGTTAGACGCCACCGTGCAGGAAAC	5520
5521	CTCGAGACTCGGTGGAAGGGACCTTATCTCGTACTTTGACCACACCAACGGCTGTGAAA	5580
5581	GTGGAAGGAATCCCCACCTGGATCCATGCATCCCACGTTAAGCYGGCGCCACCTCCCGAC	5640
5641	TGGGGTGGAGAGCCGAAAAGActGAGAATCCCCTAACGCTCGCTCCATCGCTGGTT	5700
5701	CCTTAECTAACAAATAACTCCCCAGGCCAGTAGTAAACGCCCTATAGACAGCTCGAACCC	5760
5761	CCATAGACCTTTATCCCTTACCTGGCTGATTATTGACCCCTGATAACGGGTGTCAGTGTAAA	5820
5821	TAGCACTCGAGGTGTTGCTCTAGAGGCACCTGGTGGCCTGAAGTGCATTCTGCCTCCG	5880
5881	ATTGATTAACCCCGCTGTTAARAGCACACCTCCAACCTAGTCCGTAGTTATGGGTTCTA	5940
5941	TTGCTGCCAGGCACAGAGAAAGAGAAATACTGTGGGGTTCTGGGAATCCTCTGTAG	6000
6001	GAGATGGAGCTCGGTACCTCCAAACGATGGAGACTGGAAATGCCGATCTCTCCAGGA	6060
6061	CCGGGTAAAATTCTCCTTGTCAATTCCGGCCGGCAAGTACAAAATGATGAAACTATA	6120
6121	TAAAGATAAGAGCTGCTCCCCATCAGACTTAGATTATCTAAAGATAAGTTCACTGAAAG	6180
6181	AAAAACAGGAAAATATTCAAAAGTGGATAAAATGGTATGAGCTGGGAATAGTTTTTATT	6240
6241	ATATGGCGGGGGAGCAGGGTCCACTTTAACCAATTGCCCTAGGATAGAGACGGGGACAGA	6300

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Figure 2 cont.

6301	ACCCCCCTGTGGCAATGGGACCCGATAAAAGTACTGGCTGAACAGGGGCCCGGCCCTGGA	6360
6361	GCCACCGCATAACTTGCCGGTGCCCCAATTAAACCTCGCTGCCGCCTGACATAACACAGCC	6420
6421	GCCTAGCAACAGTACCACTGGATTGATTCTACCAACACGCCTAGAAACTCCCCAGGTGT	6480
6481	TCCTGTTAACAGACAGGACAGAGACTCTTCAGTCTCATCCAGGGAGCTTCCAAGCCATCAA	6540
6541	CTCCACCGACCCTGATGCCACTTCTTCTTGGCTTGTCTATCCTCAGGGCCTCTTA	6600
6601	TTATGAGGGGATGGCTAAAGAAAAGAAAATTCAATGTGACCAAAGAGGCATAGAAATCAATG	6660
6661	TACATGGGGTCCCGAAATAAGCTTACCCCTCACTGAAGTTCCGGAAAGGGGACATGCAT	6720
6721	AGGAAGCTCCCCATCCCACCAACACCTTGCTATAGTACTGTGGTTATGAGCAGGC	6780
6781	CTCAGAAAATCAGTATTTAGTACCTGGTTATAACAGGTGGTGGCATGCAATACTGGTT	6840
6841	AACCCCCCTGTGTTCCACCTCAGTCTCAACCAATCCAAAGATTCTGTGTATGGTCCA	6900
6901	AATCGTCCCCCGAGTGTACTACCATCCTGAGGAAGTGGTCCTGATGAATAATGACTATCG	6960
6961	GTATAACCGACCAAAAGAGAACCCGTATCCCTACCCCTAGCTGTAATGCTCGGATTAGG	7020
7021	GACGGCCGTTGGCGTAGGAACAGGGACAGCTGCCCTGATCACAGGACCACAGCAGCTAGA	7080
7081	GAAAGGACTTGGTGAGCTACATGCGGCCATGACAGAAGATCTCCGAGCCTAAAGGAGTC	7140
7141	TGTTAGCAACCTAGAAGAGTCCCTGACTTCTTGTCTGAAGTGGTTCTACAGAACCGGAG	7200
7201	GGGATTAGATCTGCTGTTCTAAGAGAAGGTGGTTATGTGCAGCCTAAAAGAAGAATG	7260
7261	TTGCTTCTATGTAGATCACTCAGGAGCCATCAGAGACTCCATGAACAAGCTTAGAAAAAA	7320
7321	GTTAGAGAGGCGTCGAAGGGAAAAGAGAGGGCTGACCAGGGTGGTTGAAGGATGGTTCAA	7380
7381	CAGGTCTCCTGGATGACCACCTGCTTCTGCTCTGACGGGCCCTAGTAGTCCTGCT	7440
7441	CCTGTTACTTACAGTTGGCCTTGCTTAATTAAATAGGTTGTCCTTGTAGAGAACG	7500
7501	AGTGAGTGCAGTCCAGATCATGGTACTTAGGCAACAGTACCAAGGCCTCTGAGCCAAGG	7560

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Figure 2 cont.

7561	AGAAAACGTGACCTCTAGCCTTCCCAGTTCTAAGATTAGAACTATTAACAAGACAAGAAGTG	7620
7621	GGGAATGAAAGGATGAAAATGCAACCTAACCCCTCCCAGAACCCAGGAAGTTAATAAAAAG	7680
7681	CTCTAAATGCCCGAATTMCAGACCCTGCTGGCTGCCAGTAAATAGGTAGAAGGTCACA	7740
7741	CTTCCTATTGTTCCAGGGCTGCTATCCTGGCTAAGTAAGATAACAGGAAATGAGTTGA	7800
7801	CTAATCGCTTATCTGGATTCTGTAAAACGTGACTGGCACCATAGAAGAATTGATTACACAT	7860
7861	TGACAGCCCTAGTGACCTATCTCAACTGCAATCTGTCACTCTGCCAGGAGCCCACGCAG	7920
7921	ATGCGGACCTCCGGAGCTATTTAAAAATGATTGGTCCACGGAGCGCGGGCTCTCGATATT	7980
7981	TTAAAATGATTGGTCCATGGAGCGCGGGCTCTCGATATTTAAAATGATTGGTTGTGAC	8040
8041	GCACAGGCTTGTGAACCCATAAAAGCTGTCCCGATTCCGCACTGGGGCCGCAGT	8100
8101	CCTCTACCCCTGCGTGGTGTACGACTGTGGGCCAGCGCGCTTGGAAATAAAATCCTCT	8160
8161	TGCTGTTGCATAAAAAAAAAAAAAAAAAAAAA 8196	

Figure 3

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1	GTGGTGTACGACTGTGGGCCAGCGCGCTTGAATAAAATCCTCTGCTGTTGCATC	60
61	AAGACCGCTTCGTGAGTGATTGGGGTGTGCCTCTCCGAGCCGGACGAGGGGAT	120
121	TGTTCTTTACTGGCCTTCATTGGTGCCTGGCCGGAAATCCTGCGACCACCCCTTA	180
181	CACCCGAGAACCGACTTGGAGGTAAAGGGATCCCCTTGGAACGTGTGTGTGGCC	240
241	GGCGTCTCTGTTCTGAGTGTCTGTTGGTGTGCCTTCGGTTGCAGCTGTCCT	300
301	CTCAGACCGTAAGGACTGGAGGACTGTGATCAGCAGACGTGCTAGGAGGATCACAGGCTG	360
361	CCACCCCTGGGGACGCCCCGGAGGTGGGAGAGCCAGGGACGCCGGTGGTCTCTACT	420
421	GTCGGTCAGAGGACCGAGTTCTGTTGAAAGCGAAAGCTCCCCCTCCGGCCGTCCG	480
481	ACTCTTTGCCTGCTTGTGGAAGACGCCGGACGGTCCGTGTGTCTGGATCTGTTGGTT	540
541	CTGTCTCGTGTCTTGTCTTGTGCGTCCTGTCTACAGTTAATATGGACAGACAG MetGlyGlnThrV	600
601	TGACTACCCCCCTTAGTTGACTCTGACCATGGACTGAAGTTAGATCCAGGGCTCATA alThsThsProLeuSerLeuThrLeuAspHisTrpThrGluValArgSerArgAlaHisA	660
661	ATTTGTCAAGTTCAAGTTAAGAAGGGACCTTGGCAGACTTCTGTGCCTCTGAATGCCAA snLeuSerValGlnValLysLysGlyProTrpGlnThrPheCysAlaSerGluTrpProt	720
721	CATTCGATGTTGGATGCCATCAGAGGGACCTTAATTCTGAAATTATCCTGGCTGTTA hrPheAspValGlyTrpProSerGluGlyThrPheAsnSerGluIleIleLeuAlaValL	780
781	AGGCAATCATTTTCAGACTGGACCCGGCTCTCATCCTGATCAGGAGCCCTATATCCTTA ysAlaIleIlePheGlnThsGlyProGlySerHisProAspGlnGluProTyrIleLeut	840
841	CGTGGCAAGATTGGCAGAAGATCCTCCGCCATGGTTAAACCATGGCTAAATAACCAA hrTrpGlnAspLeuAlaGluAspProProProTrpValLysProTrpLeuAsnLysProA	900
901	GAAAGCCAGGTCCCCGAATCCTGGCTCTGGAGAGAAAAACAAACACTGGCCGAAAAG rgLysProGlyProArgIleLeuAlaLeuGlyGluLysAsnLysHisSerAlaGluLysV	960
961	TCGAGCCCTCTCCTCGTATCTACCCCGAGATCGAGGGAGCCGCCGACTTGGCCGGAACCC alGluProSerSerSerTyrLeuProArgAspArgGlyAlaAlaAspLeuAlaGlyThrP	1020
1021	CAACCTGTTCCCCACCCCTTATCCAGCACAGGGTGCTGTGAGGGGACTCTGCCCTC roThsCysSerProThrProLeuSerSerThrGlyCysCysGluGlyThrSerAlaProP	1080

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Figure 3 cont.

1081	CTGGAGCTCCGGTGGAGGGACCTGCTGCCGGACTCGGAGGCCGGAGAGGCCACCC roGlyAlaProValValGluGlyProAlaAlaGlyThrArgSerArgArgGlyAlaThrP	1140
1141	CGGAGCGGACAGACGAGATCGCGATATTACCGCTGCGCACCTATGGCCCTCCATGCCAG roGluArgThrAspGluIleAlaIleLeuProLeuArgThrTyrGlyProProMetProG	1200
1201	GGGGCCAATTGCAGCCCCCTCCAGTATTGGCCCTTTCTTCTGCAGATCTCTATAATTGGA lyGlyGlnLeuGlnProLeuGlnTyrTrpProPheSerSerAlaAspLeuTyrAsnTspL	1260
1261	AAACTAACCATCCCCCTTCCTGGAGGATCCCCAACGCCTCACGGGGTTGGTGGAGTCCC ysThrAsnHisProProPheSerGluAspProGlnArgLeuThrGlyLeuValGluSerL	1320
1321	TTATGTTCTCTCACCAGCCTACTTGGGATGATTGTCAACAGCTGCTGCAGACACTCTTCR euMetPheSerHisGlnProThrTrpAspAspCysGlnGlnLeuGlnThrLeuPheT	1380
1381	CAACCGAGGAGCGAGAGAGAATTCTGTTAGAGGCTAGAAAAAAATGTTCTGGGGCCGACG hrThrGluGluArgGluArgIleLeuLeuGluAlaArgLysAsnValProGlyAlaAspG	1440
1441	GGCGACCCACGCAGTTGCAAAATGAGATTGACATGGGATTCCCTTGACTCGCCCCGGTT lyArgProThrGlnLeuGlnAsnGluIleAspMetGlyPheProLeuThrArgProGlyT	1500
1501	GGGACTACAACACGGCTGAAGGTAGGGAGAGCTTGAAAATCTATGCCAGGCTCTGGTGG rPAspTyrAsnThrAlaGluGlyArgGluSerLeuLysIleTyrArgGlnAlaLeuValA	1560
1561	CGGGTCTCGGGGGCGCCTCAAGACGGCCCCTAATTGGCTAAGGTAAGAGAGGGTGTGC laGlyLeuArgGlyAlaSerArgArgProThrAsnLeuAlaLysValArgGluValMetG	1620
1621	AGGGACCGAACGAACTCCCTCGGTATTCTTGAGAGGCTCATGGAAGCCTTCAGGCAGG lnGlyProAsnGluProProSerValPheLeuGluArgLeuMetGluAlaPheArgArg?	1680
1681	TCACCCCTTGATCCTACCTCAGAGGCCAGAAAGCCTCAGTGGCCCTGGCCTTCATTG heThrProPheAspProThrSerGluAlaGlnLysAlaSerValAlaLeuAlaPheIleG	1740
1741	GGCAGTCGGCTCTGGATATCAGGAAGAAACTTCAGAGACTGGAAGGGTTACAGGAGGCTG lyGlnSerAlaLeuAspIleArgLysLysLeuGlnArgLeuGluGlyLeuGlnGluAlaG	1800
1801	AGTTACGTGATCTAGTGAGAGAGGCAGAGAAGGTGTATTACAGAAGGGAGACAGAAGAGG luLeuArgAspLeuValArgGluAlaGluLysValTyrTyrArgArgGluThrGluGluG	1860
1861	AGAAGGAACAGAGAAAAGAAAAGGAGAGAGAAGAAAGGGAGGAAAGACGTGATAGACGGC luLysGluGlnArgLysGluLysGluArgGluGluArgGluGluArgArgAspArgArgG	1920
1921	AAGAGAAGAATTGACTAAGATCTTGGCCGCAGTGGTTGAAGGGAAGAGCAGCAGGGAGA lnGluLysAsnLeuThrLysIleLeuAlaAlaValValGluGlyLysSerSerArgGluA	1980
1981	GAGAGAGAGATTAGGAAAATTAGGTAGGCCCTAGACAGTCAGGGAACCTGGCAATA rgGluArgAspPheArgLysIleArgSerGlyProArgGlnSerGlyAsnLeuGlyAsnA	2040

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Figure 3 cont

2041	GGACCCCACTCGACAAGGACCAGTGTGCGTATTGTAAAGAAAAAGGACACTGGGCAAGGA rgThrProLeuAspLysAspGlnCysAlaTyrCysLysGluLysGlyHisTrpAlaArgA	2100
2101	ACTGCCCAAGAAGGGAAACAAAGGACCGAAGgTCCTAGCTCTAGAAGAAGATAAAGATT snCysProLysLysGlyAsnLysGlyProLysValLeuAlaLeuGluGluAspLysAspE	2160
2161	AGGGGAGACGGGgTTCGGACCCCTCCCCGAGCCCAGGGTAACTTGAAGGTGGAGGGC ndGlyArgArgGlySerAspProLeuProGluProArgValThrLeuLysValGluGlyG	2220
2221	AACCAGTTGAGTCCTGGTGATACGGAGCGGAGCATTCACTGCTGCTACAACCATTAG lnProValGluPheLeuValAspThrGlyAlaGluHisSerValLeuLeuGlnProLeuG	2280
2281	GAAAActAAAAGAAAAAAATCCTGGGTGATGGGTGCCACAGGGCACGGCAGTATCCAT lyLysLeuLysGluLysLysserTrpValMetGlyAlaThrGlyGlnArgGlnTyrProT	2340
2341	GGACTACCCGAAGAACCGTTGACTTGGGAGTGGGACGGGTAACCCACTCGTTCTGGTCA rpThrThrArgArgThrValAspLeuGlyValGlyArgValThrHisSerPheLeuValI	2400
2401	TCCCTGAGTGCcAGTACCCCTTAGGTAGAGACTTACTGACCAAGATGGGAGCTCAA leProGluCysProValProLeuLeuGlyArgAspLeuLeuThrLysMetGlyAlaGlnI	2460
2461	TTTCTTTGAACAAGGAAGACCAGAAGTGTCTGTGAATAACAAACCCATCACTGTGTTGA leSerPheGluGlnGlyArgProGluValSerValAsnAsnLysProIleThrValLeut	2520
2521	CCCTCCAATTAGATGATGAATATCGACTATATTCTCCCCAAGTAAAGCCTGATCAAGATA hrLeuGlnLeuAspAspGluTyrSerProGlnValLysProAspGlnAspI	2580
2581	TACAGTCTGGTGGAGCAGTTCCCCAACGCTGGCAGAAACCGCAGGGATGGGTTGG leGlnSerTrpLeuGluGlnPheProGlnAlaTrpAlaGluThrAlaGlyMetGlyLeuA	2640
2641	CAAAGCAAGTCCCCACAGGTTATTCAACTGAAGGCCAGTGCTACACCAGTATCAGTCA laLysGlnValProProGlnValIleGlnLeuLysAlaSerAlaThrProValSerValA	2700
2701	GACAGTACCCCTTGAGTAGAGAGGGCTCGAGAAGGAATTGGCCGCATGTTCAAAGATTAA rgGlnTyrProLeuSerArgGluAlaArgGluGlyIleTrpProHisValGlnArgLeuI	2760
2761	TCCACAGGGCATCCTAGTTCTGTCCAATCCCCCTGGAATACTCCCCCTGCTACCGGTTA leGlnGlnGlyIleLeuValProValGlnSerProTrpAsnThrProLeuLeuProValA	2820
2821	GGAAAGCCTGGGACCAATGATTATCGACCAAGTACAGGACTTGAGAGAGGGTCAATAAAAGGG rgLysProGlyThrAsnAspTyrArgProValGlnAspLeuArgGluValAsnLysArgV	2880
2881	TGCAGGACATAACCCAACGGTCCCGAACCTTATAACCTCTTGAGCGCCCTCCCGCCTG alGlnAspIleHisProThrValProAsnProTyrAsnLeuLeuSerAlaLeuProProG	2940
2941	AACGGAACCTGGTACACAGTATTGGACTAAAAGATGCCTTCTTGAGCCTGAGATTACACC luArgAsnTrpTyrThrValLeuAspLeuLysAspAlaPhePheCysLeuArgLeuHisP	3000

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Figure 3 cont.

3001	CCACTAGCCAACCAC TTTTGCCTTCGAATGGAGAGATCCAGGTACGGGAAGAACCGGGC roThrSerGlnProLeuPheAlaPheGluTrpArgAspProGlyThrGlyArgThrGlyG	3060
3061	AGCTCACCTGGACCCGACTGCCCAAGGGTTCAAGAACTCCCCGACCATCTTGACGAAG InLeuThrTrpThrArgLeuProGlnGlyPheLysAsnSerProThrIlePheAspGluA	3120
3121	CCCTACACAGGGACCTGGCCA ACTTCAGGATCCAACACCCCTCAGGTGACCCCTCCTCCAGT laLeuHisArgAspLeuAlaAsnPheArgIleGlnHisProGlnValThrLeuLeuGlnT	3180
3181	ACGTGGATGACCTGCTTCTGGCGGGAGCCACCAAACAGGACTGCTTAGAAGGTACGAAGG yrValAspAspLeuLeuAlaGlyAlaThrLysGlnAspCysLeuGluGlyThrLysA	3240
3241	CACTACTGCTGGAATTGTCTGACCTAGGCTACAGAGCCTCTGCTAAGAAGGCCAGATT laLeuLeuLeuGluLeuSerAspLeuGlyTyrArgAlaSerAlaLysLysAlaGlnIleC	3300
3301	GCAGGAGAGAGGTAACATACTGGGGTACAGTTGCAGGGGGCAGCGATGGCTGACGG ysArgArgGluValThrTyrLeuGlyTyrSerLeuArgGlyGlyGlnArgTrpLeuThrG	3360
3361	AGGCACGGAAGAAA ACTGTAGTCCAGATA CCGGCCCCAACACAGCCAAACAAGTGAGAG luAlaArgLysLysThrValValGinIleProAlaProThrThrAlaLysGlnValAlaG	3420
3421	AGTTTTGGGGACAGCTGGATTTCAGACTGTGGATCCCAGGGTTTGCACCTAGCAG luPheLeuGlyThrAlaGlyPheCysArgLeuTrpIleProGlyPheAlaThrLeuAlaA	3480
3481	CCCCACTCTACCGCTAACCAAAGAAAAAGGGGGATTCTCCTGGCTCCTGAGCACCA laProLeuTyrProLeuThrLysGluLysGlyGlyPheSerTrpAlaProGluHisGlnL	3540
3541	AGGCATTGATGCTATCAAAAAGGCCCTGCTGAGCGCACCTGCTCTGGCCCTCCCTGACG ysAlaPheAspAlaIleLysLysAlaLeuLeuSerAlaProAlaLeuAlaLeuProAspV	3600
3601	TAACTAAACCCCTTACCCCTTATGTGGATGAGCGTAAGGGAGTAGCCCGAGGAGTTTAA alThrLysProPheThrLeuTyrValAspGluArgLysGlyValAlaArgGlyValLeuT	3660
3661	CCCAAACCCTAGGACCATGGAGGGAGACCTGTTGCCCTACCTGTCAAAGAACGCTTGATCCTG hrGlnThrLeuGlyProTrpArgArgProValAlaTyrLeuSerLysLysLeuAspProV	3720
3721	TAGCCAGTGGTTGGCCCGTATGTCTGAAGGCTATCGCAGCTGTGCCATACTGGTCAAGG alAlaSerGlyTrpProValCysLeuLysAlaIleAlaAlaValAlaIleLeuValLysA	3780
3781	ACGCTGACAAATTGACTTTGGGACAGAAATATAACTGTAATAGCCCCCATGCATTGGAGA spAlaAspLysLeuThrLeuGlyGlnAsnIleThrValIleAlaProHisAlaLeuGlnA	3840
3841	ACATCGTTGGCAGCCCCCAGACCGATGGATGACCAACGCCGCATGACCCACTATCAA snIleValArgGlnProProAspArgTrpMetThrAsnAlaArgMetThrHisTyrGlnS	3900
3901	GCCTGCTTCTCACAGAGAGGGTCACTTTCGCTCCACAGCCGCTCTCAACCCCTGCCACTC erLeuLeuLeuThrGluArgValThrPheAlaProProAlaAlaLeuAsnProAlaThrL	3960

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Figure 3 cont

3961	TTCTGCCCTGAAGAGACTGATGAACCAGTGACTCATGATTGCCATCAACTATTGATTGAGG euLeuProGluGluThrAspGluProValThrHisAspCysHisGlnLeuLeuIleGluG	4020
4021	AGACTGGGGTCCGCAAGGACCTTACAGACATACCGCTGACTGGAGAAGTGCTAACCTGGT luThrGlyValArgLysAspLeuThrAspIleProLeuThrGlyGluValLeuThrTrpP	4080
4081	TCACTGACGGAAGCAGCTATGTGGTGGAAAGGTAAGAGGGATGGCTGGGGCGGCAGTGGTGG heThrAspGlySerSerTyrValValGluGlyLysArgMetAlaGlyAlaAlaValValA	4140
4141	ACGGGACCCGCACGATCTGGGCCAGCAGCCTGCCGGAAAGGAACTTCAGCGCAAAAGGCTG spGlyThrArgThrIleTrpAlaSerSerLeuProGluGlyThrSerAlaGlnLysAlaG	4200
4201	AGCTCATGGCCCTCACGCAAGCTTGGCGCTGGCCGAAGGGAAATCCATAAACATTTATA luLeuMetAlaLeuThrGinAlaLeuArgLeuAlaGluGlyLysSerIleAsnIleTyrT	4260
4261	CGGACAGCAGGTATGCCCTTGCAGACTGCACACGTACACGGGCCATCTATAAACAAAGGG hrAspSerArgTyrAlaPheAlaThrAlaHisValHisGlyAlaIleTyrLysGlnArgG	4320
4321	GGTTGCTTACCTCAGCAGGGAGGGAAATAAGAACAAAGAGGGAAATTCTAACCTATTAG lyLeuLeuThrSerAlaGlyArgGluIleLysAsnLysGluGluIleLeuSerLeuLeuG	4380
4381	AAGCCTTACATTGCCAAAAAGGCTAGCTATTACACTGTCTGGACATCAGAAAGCCA luAlaLeuHisLeuProLysArgLeuAlaIleIleHisCysProGlyHisGlnLysAlaL	4440
4441	AAGATCTCATATCTAGAGGGAAACCAGATGGCTGACCGGGTTGCCAACGCAGGCCAGG ysAspLeuIleSerArgGlyAsnGlnMetAlaAspArgValAlaLysGlnAlaAlaGlnA	4500
4501	CTGTTAACCTCTGCCCTATAATAGAAACGCCAAAGCCCCAGAACCCAGACGACAGTACA laValAsnLeuLeuProIleIleGluThrProLysAlaProGluProArgArgGlnTyrT	4560
4561	CCCTAGAAGACTGCCAAGAGATAAAAAGATAGACCAGTTCTCTGAGACTCCGGAGGGGA hrLeuGluAspTrpGlnGluIleLysLysIleAspGlnPheSerGluThrProGluGlyT	4620
4621	CCTGCTATACCTCATATGGGAAGGGAAATCCTGCCCCACAAAGAACGGTTAGAATATGTCC hrCysTyrThrSerTyrGlyLysGluIleLeuProHisLysGluGlyLeuGluTyrValG	4680
4681	AACAGATAACATCGCTAACCCACCTAGGAACCTAACACACCTGCAGCAGTTGGTCAGAACAT lnGlnIleHisArgLeuThrHisLeuGlyThrLysHisLeuGlnGlnLeuValArgThrs	4740
4741	CCCCTTATCATGTTCTGAGGCTACCAAGGAGTGGCTGACTCGGTGGTCAAACATTGTGTGC erProTyrHisValLeuArgLeuProGlyValAlaAspSerValValLysHisCysValP	4800
4801	CCTGCCAGCTGGTTAATGCTAATCCTTCCAGAACATCCAGGAAAGAGACTAAGGGGAA roCysGlnLeuValAsnAlaAsnProSerArgIleProProGlyLysArgLeuArgGlyS	4860
4861	GCCACCCAGGCGCTCACTGGGAAGTGGACTTCAGTGAGGTAAAGCCGGCTAAATACGGAA erHisProGlyAlaHisTrpGluValAspPheThrGluValLysProAlaLysTyrGlyA	4920

Figure 3 cont.

4921 ACAAAATATCTATTGGTTTTGTAGACACCTTTCAGGATGGGTAGAGGCTTATCCTACTA 4980  
snLysTyrLeuLeuValPheValAspThrPheSerGlyTrpValGluAlaTyrProThrL

4981 AGAAAAGAGACTTCAACC GTGGTGGCTAAGAAAATACTGGAGGAAATTTTCCAAGATTG 5040  
ysLysGluThrSerThrValValAlaLysIleLeuGlugluIlePheProArgPheG

5041 GAATACCTAAGGTAA TAGGGTCAGACAATGGTCCAGCTTCGTTGCCAGGTAAAGTCAGG 5100  
lyIleProLysValIleGlySerAspAsnGlyProAlaPheValAlaGlnValSerGlnG

5101 GACTGGCCAAGATATTGGGGATTGGATTGGAAACTGCATTGTGCATAACAGACCCCCAAAGCT 5160  
lyLeuAlaLysIleLeuGlyIleAspTrpLysLeuHisCysAlaTyrArgProGlnSerS

5161 CAGGACAGGTAGAGAGGGATGAATAGAACCATTAAGAGACCCCTTACCAAATTGACCACAG 5220  
erGlyGlnValGluArgMetAsnArgThrIleLysGluThrLeuThrLysLeuThrThrG

5221 AGACTGGCATTAAATGATTGGATGGCTCTCCCTGCCCTTGCTGCTTTAGGGTGAGGAACA 5280  
luThrGlyIleAsnAspTrpMetAlaLeuLeuProPheValLeuPheArgValArgAsnT

5281 CCCCTGGACAGTTGGCTGACCCCCCTATGAATTGCTCTACGGGGGACCCCCCCCCTTGG 5340  
hrProGlyGlnPheGlyLeuThrProTy rGluLeuLeuTy rGlyGlyProProProLeuA

5341 CAGAAAATGCCTTGCACATAGTGCTGATGTGCTGCTTCCCAGCCTTGTCTCTAGGC 5400  
laGluIleAlaPheAlaHisSerAlaAspValLeuLeuSerGlnProLeuPheSerArgL

5401 TCAAGGGCGCTCGAGTGGGTGAGGCAGCGAGCGTGGAAAGCAGCTCCGGGAGGCCTACTCAG 5460  
euLysAlaLeuGluTrpValArgGlnArgAlaTrpLysGlnLeuArgGluAlaTyrSerG

5461 GAGGAGACTTGCAGATTCCACATCGCTTCAAGTTGGAGATTCACTCTATGTTAGACGCC 5520  
lyGlyAspLeuGlnValProHisArgPheGlnValGlyAspSerValTyrValArgArgH

5521 ACCGTGCAGGAAACCTCGAGACTCGGTGGAAGGGACCTTATCTCGTACTTTGACCACAC 5580  
isArgAlaGlyAsnLeuGluThrArgTrpLysGlyProTyrLeuValLeuLeuThrThrP

5581 CAACGGCTGTGAAAGTCGAAGGAATCCCCACCTGGATCCATGCATCCPACGTTAACGCCGG 5640  
roThrAlaValLysValGluGlyIleProThrTrpIleHisAlaSerHisValLysProA  
MetHisProThrLeuSerArg

5641 CGCCACCTCCCGACTCGGGGTGGAGAGCGAAAAGActTGAGAATCCCCCTAACGCTTCGCC 5700  
laProProProAspSerGlyTrpArgAlaGluLysThrGluAsnProLeuLysLeuArgL  
ArgHisLeuProThrArgGlyGlyGluProLysArgLeuArgIleProLeuSerPheAla

5701 TCCATCGCCTGGTTCTTACTCTAACAAACTCCCCAGGCCAGTAGTAAACGCCCTTATA 5760  
euHisArgLeuValProTyrSerAsnAsnAsnSerProGlyGlnEnd  
SerIleAlaTrpPheLeuThrLeuThrIleThrProGlnAlaSerSerLysArgLeuIle

5761 GACAGCTCGAACCCCCATAGACCTTATCCCTTACCTGGCTGATTATTGACCCCTGATACG 5820  
AspSerSerAsnProHisArgProLeuSerLeuThrTrpLeuIleIleAspProAspThr

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Figure 3 cont

5821	GGTGTCACTGTAAATAGCACTCGAGGTGTTGCTCCTAGAGGCACCTGGTGGCCTGA GlyValThrValAsnSerThrArgGlyValAlaProArgGlyThrTrpTrpProGluLeu	5880
5881	CATTTCCTGCCCTCCGATTGATTAACCCCGCTGTTAAAAGCACACCTCCAACCTAGTCCGT HisPheCysLeuArgLeuIleAsnProAlaValLysSerThrProProAsnLeuValArg	5940
5941	AGTTATGGGTTCTATTGCTGCCAGGCACAGAGAAAGAGAAATACTGTGGGGTTCTGGG SerTyrGlyPheTyrCysCysProGlyThrGluLysGluLysTyrCysGlyGlySerGly	6000
6001	GAATCCTTCTGTAGGAGATGGAGCTGCGTCACCTCCAACGATGGAGACTGGAAATGGCCG GluSerPheCysArgArgTrpSerCysValThrSerAsnAspGlyAspTrpLysTrpPro	6060
6061	ATCTCTCTCCAGGACC GG TAAAATTCTCCTTGTCATTCCGGCCC GGG CAAGTACAAA IleSerLeuGlnAspArgValLysPheSerPheValAsnSerGlyProGlyLysTyrLys	6120
6121	ATGATGAAA ACTATATAAGATAAGAGCTGCTCCCCATCAGACTTAGATTATCTAAAAGATA MetMetLysLeuTyrLysAspLysSerCysSerProSerAspLeuAspTyrLeuLysIle	6180
6181	AGTTTCACTGAAAGGAAA ACAGGAAA ATATTCAAAGTGGATAAAATGGTATGAGCTGGG SerPheThrGluArgLysThrGlyLysTyrSerLysValAspLysTrpTyrGluLeuGly	6240
6241	AATAGTTTTTATTATATGGCGGGGGAGCAGGGTCCACTTTAACCTCGCCTTAGGATA AsnSerPheLeuLeuTyrGlyGlyGlyAlaGlySerThrLeuThrIleArgLeuArgIle	6300
6301	GAGACGGGGACAGAACCCCTGTGGCAATGGGACCCGATAAAAGTACTGGCTGAACAGGG GluThrGlyThrGluProProValAlaMetGlyProAspLysValLeuAlaGluGlnGly	6360
6361	CCCCCGGCCCTGGAGCCACCGCATAACTTGCCGGTGC CCAATT AACCTCGCTGC ProProAlaLeuGluProProHisAsnLeuProValProGlnLeuThrSerLeuArgPro	6420
6421	GACATAACACAGCCGCCTAGCAACAGTACCACTGGATTGATT CCTACCAACACGCCTAGA AspIleThrGlnProProSerAsnSerThrThrGlyLeuIleProThrAsnThrProArg	6480
6481	AACTCCCCAGGTGTTCTGTTAAGACAGGACAGAGACTCTTCAGTCTCATCCAGGGAGCT AsnSerProGlyValProValLysThrGlyGlnArgLeuPheSerLeuIleGlnGlyAla	6540
6541	TTCCAAGCCATCAACTCCACCGACCCCTGATGCCACTTCTTGTGTTGGCTTGCTATCC PheGlnAlaIleAsnSerThrAspProAspAlaThrSerSerCysTrpLeuCysLeuSer	6600
6601	TCAGGGCCTCCTTATTATGAGGGGATGGCTAAAGAAAAGAAAATTCAATGTGACCAAGAG SerGlyProProTyrGluGlyMetAlaLysGluArgLysPheAsnValThrLysGlu	6660
6661	CATAGAAAATCAATGTACATGGGGGTCCGAAAATAAGCTTACCCACTGAAGTTCCGGG HisArgAsnGlnCysThrTrpGlySerArgAsnLysLeuThrLeuThrGluValSerGly	6720
6721	AAGGGGACATGCATAGGAAAAGCTCCCCATCCCACCAACACCTTGCTATAGTACTGTG LysGlyThrCysIleGlyLysAlaProProSerHisGlnHisLeuCysTyrSerThrVal	6780

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Figure 3 cont.

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6781	GTTTATGAGCAGGCCCTCAGAAAATCAGTATTTAGTACCTGGTTATAACAGGTGGTGGGCA ValTyrGluGlnAlaSerGluAsnGlnTyrLeuValProGlyTyrAsnArgTrpTrpAla	6840
6841	TGCAATACTGGGTTAACCCCTGTGTTCCACCTCAGTCTCAACCAATCCAAAGATTTC CysAsnThrGlyLeuThrProCysValSerThrSerValPheAsnGlnSerLysAspPhe	6900
6901	TGTGTCATGGTCCAAATCGTCCCCCGAGTGTACTACCATCCTGAGGAAGTGGTCCTTGAT CysValMetValGlnIleValProArgValTyrTyrHisProGluGluValValLeuAsp	6960
6961	GAATATGACTATCGGTATAACCGACCAAAAGAGAACCCGTATCCCTTACCCTAGCTGTA GluTyrAspTyrArgTyrAsnArgProLysArgGluProValSerLeuThrLeuAlaVal	7020
7021	ATGCTCGGATTAGGGACGGCCGTTGGCGTAGGAAACAGGGACAGCTGCCCTGATCACAGGA MetLeuGlyLeuGlyThrAlaValGlyValGlyThrGlyThrAlaAlaLeuIleThrGly	7080
7081	CCACAGCAGCTAGAGAAAGGACTTGGTGAGCTACATGCGGCCATGACAGAAGATCTCCGA ProGlnGlnLeuGluLysGlyLeuGlyGluLeuHisAlaAlaMetThrGluAspLeuArg	7140
7141	GCCTTAAAGGAGTCTGTTAGCAACCTAGAAGAGTCCCTGACTTCTTGCTGAAGTGGTT AlaLeuLysGluSerValSerAsnLeuGluSerLeuThrSerLeuSerGluValVal	7200
7201	CTACAGAACCGGAGGGGATTAGATCTGCTGTTCTAAGAGAACGGTGGTTATGTGCAGCC LeuGlnAsnArgArgGlyLeuAspLeuLeuPheLeuArgGluGlyGlyLeuCysAlaAla	7260
7261	TTAAAAAGAAGAATGTTGCTTCTATGTAGATCACTCAGGAGCCATCAGAGACTCCATGAAC LeuLysGluGluCysCysPheTyrValAspHisSerGlyAlaAlaArgAspSerMetAsn	7320
7321	AAGCTTAGAAAAAAAGTTAGAGAGGGCGTCGAAGGGAAAGAGAGGGCTGACCAGGGTGGTT LysLeuArgLysLysLeuGluArgArgArgGluArgAlaAspGlnGlyTyrPhe	7380
7381	GAAGGATGGTTAACAGGTCTCCTGGATGACCACCCCTGCTTCTGCTCTGACGGGGCCC GluGlyTrpPheAsnArgSerProTrpMetThrThrLeuLeuSerAlaLeuThrGlyPro	7440
7441	CTAGTAGTCCTGCTCCTGTTACTTACAGTTGGGCCTGCTTAATTAAAGGTTGGCC LeuValValLeuLeuLeuLeuThrValGlyProCysLeuIleAsnArgPheValAla	7500
7501	TTTGTAGAGAACGAGTGAGTCAGTCAGATCATGGTACTTAGGCAACAGTACCAAGGC PheValArgGluArgValSerAlaValGlnIleMetValLeuArgGlnGlnTyrGlnGly	7560
7561	CTTCTGAGCCAAGGAGAAACTGACCTCTAGCCTCCAGTTCTAAGATTAGAACTATTAA LeuLeuSerGlnGlyGluThrAspLeuEnd	7620
7621	CAAGACAAGAACGAGGGATGAAAGGATGAAATGCAACCTAACCCCTCCAGAACCCAGG	7680
7681	AAGTTAATAAAAGCTCTAAATGCCCGAATTACAGACCCCTGCTGGCTGCCAGTAAATA	7740

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Figure 3 cont.

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7741	GGTAGAAGGTACACTTCCTATTGTTCCAGGGCCTGCTATCCTGGCTAACGTAAGATAAC	7800
7801	AGGAAATGAGTTGACTAATCGCTTATCTGGATTCTGTAAAAGTGAUTGGCACCATAGAAG	7860
7861	AATTGATTACACATTGACAGCCCTAGTGACCTATCTCAACTGCAATCTGTCACTCTGCC	7920
7921	AGGAGCCCACGCAGATGCGGACCTCCGGAGCTATTTAAAATGATTGGTCCACGGAGCGC	7980
7981	GGGCTCTCGATATTTAAAATGATTGGTCCATGGAGCGCGGGCTCTCGATATTTAAAAT	8040
8041	GATTGGTTTGTGACGGCACAGGCTTGTGAAACCCATAAAAGCTGTCCCGATTCCGCA	8100
8101	CTCGGGGCCGCAGTCCTCTACCCCTGGTGGTGTACGACTGTGGGCCCCAGCGCGCTTGG	8160
8161	AATAAAAATCCTTTGCTGTTGCATCAAAAAAAAAAAAAAAA	8209

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Figure 4.

The same nucleotide sequence as represented by bases 5260 to 8210 in Figure 3 is also representative for this Figure, with the following changes:

<u>Position</u>	<u>Change</u>
5273	G-T
5341	C-T
5351	C-T
5353	T-C
5356	C-T
5426	G-A
5464	Insertion AGA
5607	C-T
5638	C-T
5792	T-C
6191	Insertion AA
6253	T-A
6255	Insertion A
6900	C-G

Such nucleotide changes result in the following amino acid changes in the ENV polypeptide.

<u>Position</u>	<u>Change</u>
7	R-W
192	R-K
193	Deletion
194	Deletion
197	Y-Q
198	S-E
199	K-N
200	V-I
201	D-Q
204	Y-I
205	E-N
206	Insertions: G, M, S
206	L-W
208	N-I
209	S-V
211	L-Y
212	L-K
427	F-L

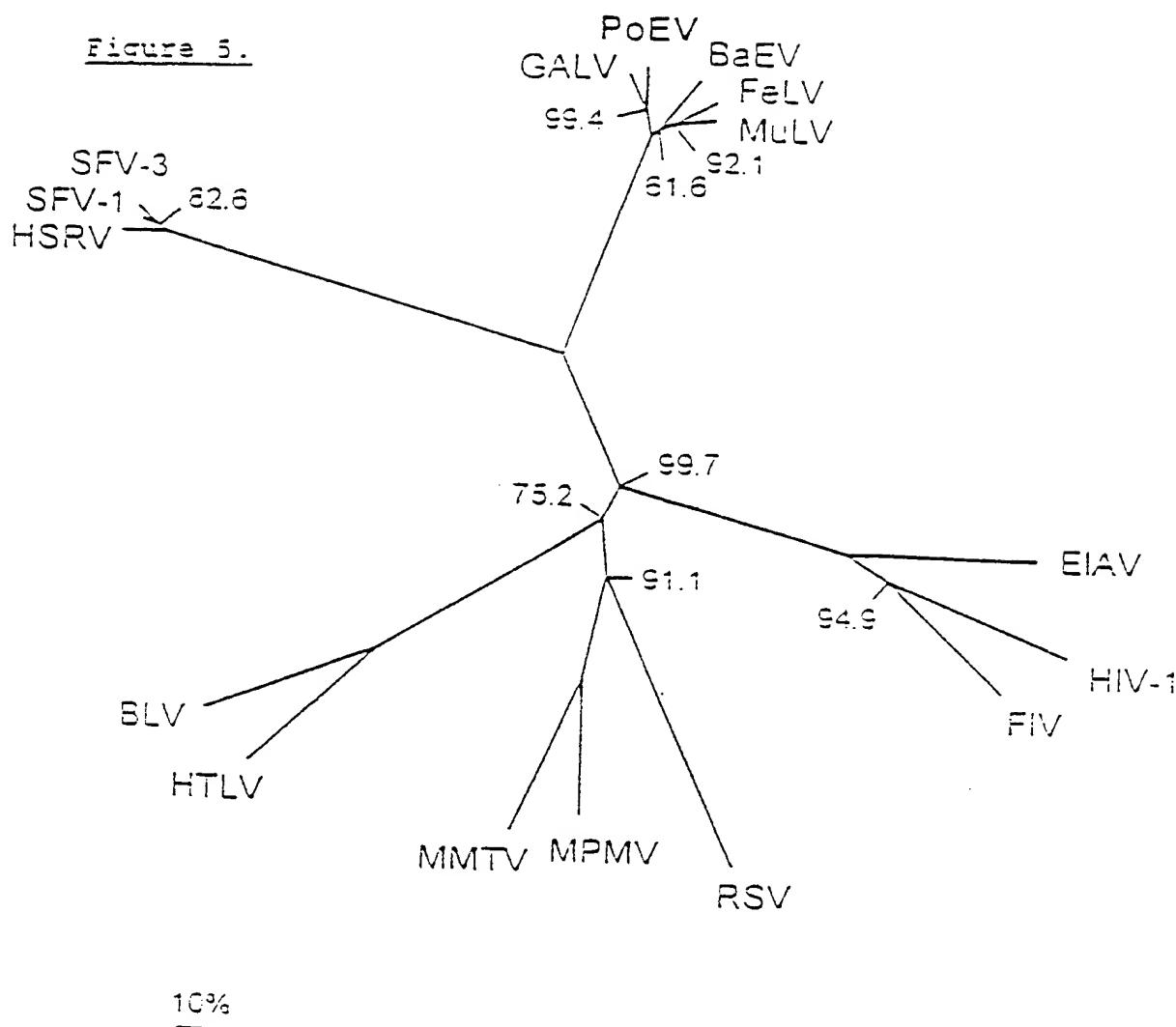
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Figure 5.



- MuLV murine leukaemia virus
- FeLV feline leukaemia virus
- GaLV gibbon ape leukaemia virus
- SVV-1 simian foamy virus 1
- SFV-3 simian foamy virus 3
- HSRV human foamy virus
- SLV Bovine leukaemia virus
- HTLV human T-cell leukaemia virus
- MMTV murine mammary tumour virus
- MPMV Mason Pfizer monkey virus
- RSV Rous sarcoma virus
- FIV feline immunodeficiency virus
- HIV human immunodeficiency virus
- EIAV equine infectious anaemia virus

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Figure 6

PPT | U3 OCT-1 c-Myb LyF-1 E47

1 AAGAAGTGGGGAAATGAAAGGATGAAAATGCAACCTAACCCCTCCCAGAAC

ETS-1 AP-4

51 CAGGAAGTTAATAAAAAGCTCTAAATGCCCGAATTMCAGACCCTGCTG

NF-1 AP-1/TR

101 GCTGCCAGTAAATAGGTAGAACGGTCACACTTCCTATTGTTCCAGGGCCTG

ETS-1/GATA GATA ETS-1 c-Myb AP-1 GATA

151 CTATCCTGGCCTAAGTAAGATAACAGGAAATGAGTTGACTAATCGCTTAT

E47 AP-1

201 CTGGATTCTGTAAAATGACTGGCACCATAGAAGAATTGATTACACATTG

AP-1 AP-1/GATA c-Myb AP-1

251 ACAGCCCTAGTGACCTATCTCAACTGCAATCTGTCACTCTGCCAGGAGC

E47 ETS-1 → CCAAT

301 CCACGCAGATGCGGACCTCCGGAGCTATTAAAATGATTGGTCCACCGGA

GATA → CCAAT ←

351 GCGCGGGCTCTCGATATTTAAAATGATTGGTCCATGGAGCGCGGGCTCT

GATA CCAAT ← AP-1/CREB

401 CGATATTTAAAATGATTGGTTGTGACGCACAGGCTTGTGAACCC

TATA U3 | R

451 CATAAAAGCTGTCCCGATTCCGACTCGGGGCCGAGTCCTCTACCCCTG

PADS polyA

501 CGTGGTGTACGACTGTGGGCCAGCGCGCTTGGAAATAAAATCCTCTTG

R | U5

551 CTGTTGCATCAAGACCGCTTCTYGTGAGTGATTGGGTGTCGCCTCTT

U5 | PBS

601 CCGAKCCCGGACGAGGGGATTGTTCTTACTGGCCTTCATTGGTGC

651 GTTGGCCGGAAATCCTGCGACC